

1/7
FIGURE 1

Nucleotide sequence and the deduced amino acid sequence of a GST-Pro-Hirudin fusion.

1	ATG TCC CCT ATA CTA GGT TAT TGG AAA ATT AAG GGC CTT GTG CAA CCC ACT CGA CTT CTT	60
1	M S P I L G Y W K I K G L V Q P T R L L	20
61	TTG GAA TAT CTT GAA GAA AAA TAT GAA GAG CAT TTG TAT GAG CGC GAT GAA GGT GAT AAA	120
21	L E Y L E E K Y E E H L Y E R D E G D K	40
121	TGG CGA AAC AAA AAG TTT GAA TTG GGT TTG GAG TTT CCC AAT CTT CCT TAT TAT ATT GAT	180
41	W R N K K F E L G L E F P N L P Y Y I D	60
181	GGT GAT GTT AAA TTA ACA CAG TCT ATG GCC ATC ATA CGT TAT ATA GCT GAC AAG CAC AAC	240
61	G D V K L T Q S M A I I R Y I A D K H N	80
241	ATG TTG GGT GGT TGT CCA AAA GAG CGT GCA GAG ATT TCA ATG CTT GAA GGA GCG GTT TTG	300
81	M L G G C P K E R A E I S M L E G A V L	100
301	GAT ATT AGA TAC GGT GTT TCG AGA ATT GCA TAT AGT AAA GAC TTT GAA ACT CTC AAA GTT	360
101	D I R Y G V S R I A Y S K D F E T L K V	120
361	GAT TTT CTT AGC AAG CTA CCT GAA ATG CTG AAA ATG TTC GAA GAT CGT TTA TGT CAT AAA	420
121	D F L S K L P E M L K M F E D R L C H K	140
421	ACA TAT TTA AAT GGT GAT CAT GTA ACC CAT CCT GAC TTC ATG TTG TAT GAC GCT CTT GAT	480
141	T Y L N G D H V T H P D F M L Y D A L D	160
481	GTT GTT TTA TAC ATG GAC CCA ATG TGC CTG GAT GCG TTC CCA AAA TTA GTT TGT TTT AAA	540
161	V V L Y M D P M C L D A F P K L V C F K	180
541	AAA CGT ATT GAA GCT ATC CCA CAA ATT GAT AAG TAC TTG AAA TCC AGC AAG TAT ATA GCA	600
181	K R I E A I P Q I D K Y L K S S K Y I A	200
601	TGG CCT TTG CAG GGC TGG CAA GCC ACG TTT GGT GGT GGC GAC CAT CCT CCA AAA TCG GAT	660
201	W P L Q G W Q A T F G G G D H P P K S D	220
661	CTG GTT CCG CGT GGA TCC CCG AAT TCC CGG GTC GAC TCG AGC GGC CGC GCT GAG ATC ACC	720
221	L V P R G S P N S R V D S S G R <u>A E I T</u>	240

2/7
FIGURE 1 (Cont'd)

721	AGG ATC CCT CTG TAC AAA GGC AAG TCT CTG AGG AAG GCG CTG AAG GAG CAT GGG CTT CTG	780
241	<u>R I P L Y K G K S L R K A L K E H G L L</u>	260
781	GAG GAC TTC CTG CAG AAA CAG CAG TAT GGC ATC AGC AGC AAG TAC TCC GGC TTC GTC GTC	840
261	<u>E D F L O K O O Y G I S S K Y S G F V V</u>	280
	↑	↑
841	TAT ACC GAC TGT ACC GAG TCC GGT CAG AAC CTC TGT CTC TGT GAG GGT TCC AAC GTC TGT	900
281	<u>Y T D C T E S G Q N L C L C E G S N V C</u>	300
901	GGT CAG GGT AAC AAG TGT ATC CTC GGT TCC GAC GGT GAG AAG AAC CAG TGT GTC ACC GGT	960
301	<u>G Q G N K C I L G S D G E K N Q C V T G</u>	320
961	GAG GGA ACC CCA AAG CCA CAG TCC CAC AAC GAC GGT GAC TTT GAG GAG ATC CCA GAG GAG	1020
321	<u>E G T P K P Q S H N D G D F E E I P E E</u>	340
1021	TAT CTC CAG TAA agatctaagcttgctgctgctatcgaattcctgcagcccggggatccactagttctagagcgg	1096
341	<u>Y L Q *</u>	344

3/7
FIGURE 2

Nucleotide sequence and the deduced amino acid sequence of a His-Pro-cGH fusion.

Poly Histidine Site

1 ATG CGG GGT TCT CAT CAT CAT CAT CAT CAT GGT ATG GCT AGC ATG ACT GGT GGA CAG CAA 60
1 M R G S H H H H H H G M A S M T G G Q Q 20

EK recognition site

61 ATG GGT CGG GAT CTG TAC GAC GAT GAC GAT AAG GAT CCG AGC TCG AGA TCT GCA GAA ATC 120
21 M G R D L T D D D D K D P S S R S A E I 40

↑

121 GGA TCC GCT GAG ATC ACC AGG ATC CCT CTG TAC AAA GGC AAG TCT CTG AGG AAG GCG CTG 180
41 G S A E I T R I P L Y K G K S L R K A L 60

181 AAG GAG CAT GGG CTT CTG GAG GAC TTC CTG CAG AAA CAG CAG TAT GGC ATC AGC AGC AAG 240
61 K E H G L L E D F L Q K Q Q Y G I S S K 80

241 TAC TCC GGC TTC TCA GAC AAC CAG CGG CTC TTC AAT AAT GCA GTC ATT CGT GTA CAA CAC 300
81 Y S G F S D N Q R L F N N A V I R V Q H 100

↑

301 CTG CAC CAG CTG GCT GCA AAA ATG ATT AAC GAC TTT GAG GAC AGC CTG TTG CCT GAG GAA 360
101 L H Q L A A K M I N D F E D S L L P E E 120

361 CGC AGA CAG CTG AGT AAA ATC TTC CCT CTG TCT TTC TGC AAT TCT GAC TAC ATT GAG GCG 420
121 R R Q L S K I F P L S F C N S D Y I E A 140

421 CCT GCT GGA AAA GAT GAA ACA CAG AAG AGC TCT ATG CTG AAG CTT CTT CGC ATC TCT TTT 480
141 P A G K D E T Q K S S M L K L L R I S F 160

481 CAC CTC ATT GAG TCC TGG GAG TTC CCA AGC CAG TCC CTG AGC GGA ACC GTC TCA AAC AGC 540
161 H L I E S W E F P S Q S L S G T V S N S 180

541 CTG ACC GTA GGG AAC CCC AAC CAG CTC ACT GAG AAG CTG GCC GAC TTG AAA ATG GGC ATC 600
181 L T V G N P N Q L T E K L A D L K M G I 200

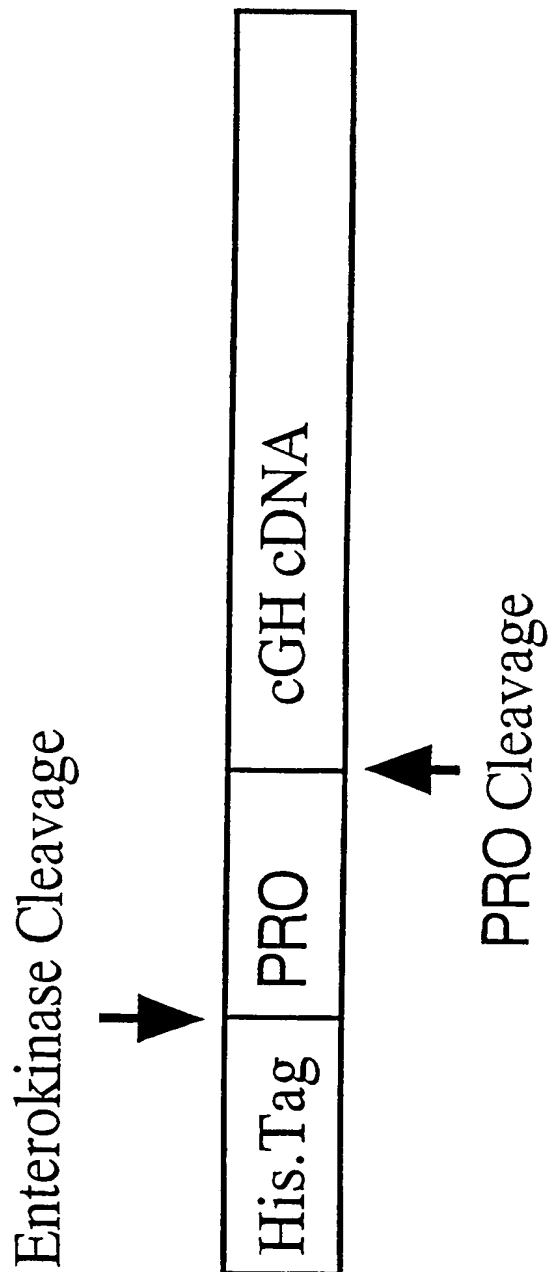
4/7FIGURE 2 (Cont'd)

601 AGT GTG CTC ATC CAG GCA TGT CTC GAT GGT CAA CCA AAC ATG GAT GAT AAC GAC TCC TTG 660
201 S V L I Q A C L D G Q P N M D D N D S L 220

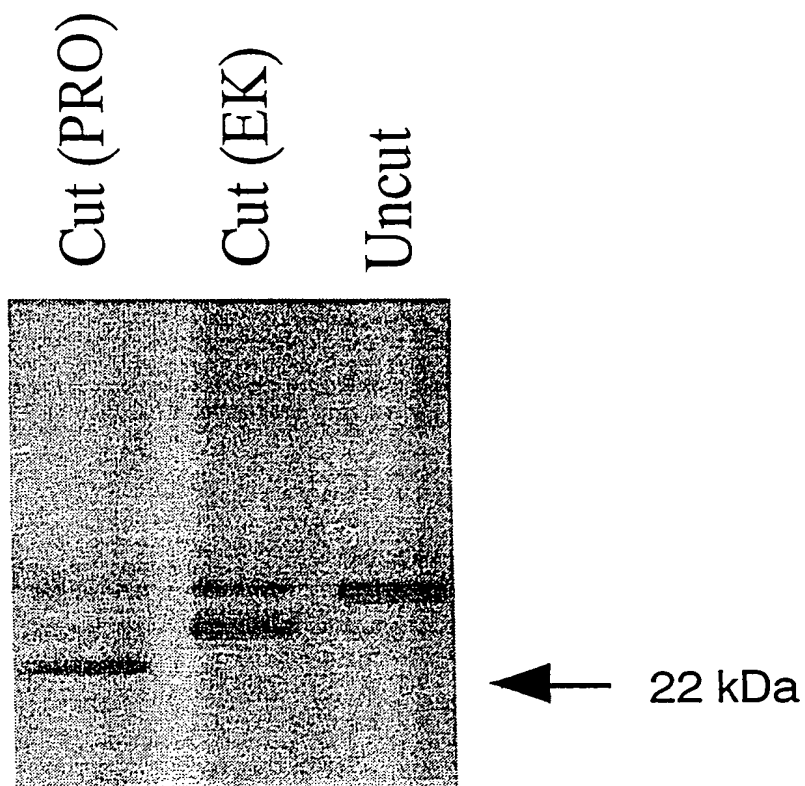
661 CCG CTG CCT TTT GAG GAC TTC TAC TTG ACC ATG GGG GAG AAC AAC CTC AGA GAG AGC TTT 720
221 P L P F E D F Y L T M G E N N L R E S F 240

721 CGT CTG CTG GCT TGC TTC AAG AAG GAC ATG CAC AAA GTC GAG ACC TAC TTG AGG GTT GCA 780
241 R L L A C F K K D M H K V E T Y L R V A 260

781 AAT TGC AGG AGA TCC CTG GAT TCC AAC TGC ACC CTG TAG
261 N C R R S L D S N C T L *

5/7FIGURE 3

6 / 7
FIGURE 4



7/7
FIGURE 5

